

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/901,938

DATE: 07/25/2001

TIME: 14:05:24

Input Set : A:\053884-5001.ST25.txt

Output Set: N:\CRF3\07252001\I901938.raw

ENTERED

3 <110> APPLICANT: ECONS, Michael
 4 WHITE, Kenneth
 5 STROM, Tim
 6 MEITINGER, Thomas
 8 <120> TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
 10 <130> FILE REFERENCE: 053884-5001
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/901,938
 C--> 13 <141> CURRENT FILING DATE: 2001-07-10
 15 <150> PRIOR APPLICATION NUMBER: 60/219,137
 16 <151> PRIOR FILING DATE: 2000-07-19
 18 <160> NUMBER OF SEQ ID NOS: 34
 20 <170> SOFTWARE: PatentIn version 3.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1612
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
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 32 gcaccagcca ctcagagcag ggcacgatgt tggggccccg cctcaggctc tgggtctgtg 180
 34 ccttgtcagc cgtctgcagc atgagcgtcc tcagagccta tcccaatgcc tccccactgc 240
 36 tcggctccag ctggggtggc ctgatccacc tgtacacagc cacagccagg aacagctacc 300
 38 acctgcagat ccacaagaat ggcatgtgg atggcgcacc ccatcagacc atctacagtg 360
 40 ccctgtatgt cagatcagag gatgctggct ttgtggtgat tacaggttg atgagcagaa 420
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 46 atcaacttcct ggtcagtcg ggcggggcga agagagcctt ctcgcaggc atgaacccac 600
 48 cccctgtactc ccagttctg tcccggagga acgagatccc cctaattcac ttcaacaccc 660
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 54 ggcgcgagga caacagcccg atggccagtg acccattagg ggtggtcagg ggcgtcgg 840
 56 tgaacacgca cgctggggaa acggggccgg aaggctgccc cccctcgcc aagttcatct 900
 58 aggtcgtctg gaaggccacc ctcttaacc catccctcag caaacgcagc tcttccaag 960
 60 gaccagggtcc cttgacgttc cgaggatggg aaaggtgaca ggggcattgt tgaaatttgc 1020
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 74 cactggcatt tgagtgtgca aaccttgaca ttaacagctg aatggggcaa gttgatgaaa 1440
 76 acactacttt caagccttcg ttcttccttg agcatctctg gggaaagagct gtcaaaagac 1500
 78 tgggtggtagg ctggtaaaaa ctgacagct agacttgatg cttgctgaaa tgaggcagga 1560
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 83 <210> SEQ ID NO: 2
 84 <211> LENGTH: 251
 85 <212> TYPE: PRT

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 94 20 25 30
 96 Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg
 97 35 40 45
 99 Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala
 100 50 55 60
 102 Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala
 103 65 70 75 80
 105 Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met
 106 85 90 95
 108 Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn
 109 100 105 110
 111 Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His
 112 115 120 125
 114 Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala
 115 130 135 140
 117 Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg
 118 145 150 155 160
 120 Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg
 121 165 170 175
 123 His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val
 124 180 185 190
 126 Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln
 127 195 200 205
 129 Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu
 130 210 215 220
 132 Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
 133 225 230 235 240
 135 Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
 136 245 250
 138 <210> SEQ ID NO: 3
 139 <211> LENGTH: 1559
 140 <212> TYPE: DNA
 141 <213> ORGANISM: Mus sp.
 143 <400> SEQUENCE: 3
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 148 ctagagccta tccggacact tccccattgc ttggctccaa ctgggaagc ctgaccacc 180
 150 tttcacggc tacagccagg accagctatc acctacagat ccataggat ggtcatgtag 240
 152 atggcacccc ccatcagacc atctacagt ccctgtatgat tacatcagag gacgccggct 300
 154 ctgtggtgat aacaggagcc atgactcgaa gtttctttg tatggatctc cacggcaaca 360
 156 ttttggatc gtttacttc agcccagaga attgcaagtt ccggcagtg acgctggaga 420
 158 atggctatga cgtctacttg tcgcagaagc atcactacct ggtgagcctg ggccgcgcca 480
 160 agcgcacatctt ccagccggc accaaccgc cgcccttctc ccagttctg gctcgcagga 540
 162 acgaggtccc gctgctgcat ttctacactg ttcccccacg gcgccacacg cgcaagcgccg 600

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164	aggaccacc	ggagcgcgac	ccactgaacg	tgctcaagcc	gcggccccgc	gccacgcctg	660										
166	tgcctgtatc	ctgctctcg	gagctgccg	gcgcagagga	aggtggccccc	gcagccagcg	720										
168	atcctctggg	ggtgctgcgc	agaggccgtg	gagatgctcg	cgggggcgcg	ggagggcgcgg	780										
170	ataggtgtcg	cccttccc	aggttcgct	aggccccag	gccaggctgc	gtccgcctcc	840										
172	atcctccagt	cggttcagcc	cacgttagagg	aaggactagg	gtacctcgag	gatgtctgct	900										
174	tctctccctt	ccctatgggc	ctgagagtca	cctgcgaggt	tccagccagg	caccgctatt	960										
176	cagaattaag	agccaacgg	gggaggctgg	agaggtggcg	cagacaggttc	tcagcaccca	1020										
178	caaatacctg	taattcttagc	tccagggaa	tctgtactca	cacacacaca	catccacaca	1080										
180	cacacacaca	cacatacatg	taattttaaa	tgttaatctg	attnaaagac	cccaacaggt	1140										
182	aaactagaca	cgaagctctt	tttattttat	tttactaaca	ggtaaaccag	acacttggcc	1200										
184	tttatttagcc	gggtctcttg	cctagcattt	taatcgatca	gttagcacga	ggaaagagtt	1260										
186	cacgccttga	acacaggaa	gaggccatct	ctgcagcttc	tagttactat	tctgggattc	1320										
188	acgggtgttt	gagtttgagc	accttgacct	taatgtcttc	actaggcaag	tcgaagaaaag	1380										
190	acgcgcattt	cttcttttg	ggaagagctt	tggattggcg	ggaggctgac	aaggacacct	1440										
192	aaaccgaaca	catttcagag	ttcagcctcc	ctgaggaatg	attcgccaat	gattctgtga	1500										
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207	Cys	Ser	Leu	Gly	Thr	Ala	Arg	Ala	Tyr	Pro	Asp	Thr	Ser	Pro	Leu	Leu	
208					20				25								30
210	Gly	Ser	Asn	Trp	Gly	Ser	Leu	Thr	His	Leu	Tyr	Thr	Ala	Thr	Ala	Arg	
211					35				40								45
213	Thr	Ser	Tyr	His	Leu	Gln	Ile	His	Arg	Asp	Gly	His	Val	Asp	Gly	Thr	
214					50				55								60
216	Pro	His	Gln	Thr	Ile	Tyr	Ser	Ala	Leu	Met	Ile	Thr	Ser	Glu	Asp	Ala	
217	65				70				75								80
219	Gly	Ser	Val	Val	Ile	Thr	Gly	Ala	Met	Thr	Arg	Arg	Phe	Leu	Cys	Met	
220					85				90								95
222	Asp	Leu	His	Gly	Asn	Ile	Phe	Gly	Ser	Leu	His	Phe	Ser	Pro	Glu	Asn	
223					100				105								110
225	Cys	Lys	Phe	Arg	Gln	Trp	Thr	Leu	Glu	Asn	Gly	Tyr	Asp	Val	Tyr	Leu	
226					115				120								125
228	Ser	Gln	Lys	His	His	Tyr	Leu	Val	Ser	Leu	Gly	Arg	Ala	Lys	Arg	Ile	
229					130				135								140
231	Phe	Gln	Pro	Gly	Thr	Asn	Pro	Pro	Phe	Ser	Gln	Phe	Leu	Ala	Arg		
232	145				150				155								160
234	Arg	Asn	Glu	Val	Pro	Leu	Leu	His	Phe	Tyr	Thr	Val	Arg	Pro	Arg	Arg	
235					165				170								175
237	His	Thr	Arg	Ser	Ala	Glu	Asp	Pro	Pro	Glu	Arg	Asp	Pro	Leu	Asn	Val	
238					180				185								190
240	Leu	Lys	Pro	Arg	Pro	Arg	Ala	Thr	Pro	Val	Pro	Val	Ser	Cys	Ser	Arg	
241					195				200								205
243	Glu	Leu	Pro	Ser	Ala	Glu	Glu	Gly	Gly	Pro	Ala	Ala	Ser	Asp	Pro	Leu	
244					210				215								220

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246 Gly Val Leu Arg Arg Gly Arg Gly Asp Ala Arg Gly Gly Ala Gly Gly
247 225 230 235 240
249 Ala Asp Arg Cys Arg Pro Phe Pro Arg Phe Val
250 245 250
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254 <212> TYPE: PRT
255 <213> ORGANISM: Homo sapiens
257 <400> SEQUENCE: 5
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260 1 5 10 15
262 Asp
265 <210> SEQ ID NO: 6
266 <211> LENGTH: 25
267 <212> TYPE: DNA
268 <213> ORGANISM: Homo sapiens
270 <400> SEQUENCE: 6
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275 <211> LENGTH: 25
276 <212> TYPE: DNA
277 <213> ORGANISM: Homo sapiens
279 <400> SEQUENCE: 7
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285 <212> TYPE: DNA
286 <213> ORGANISM: Homo sapiens
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294 <212> TYPE: DNA
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297 <400> SEQUENCE: 9
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303 <212> TYPE: DNA
304 <213> ORGANISM: Homo sapiens
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311 <211> LENGTH: 21
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313 <213> ORGANISM: Homo sapiens
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Input Set : A:\053884-5001.ST25.txt
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348 20 25 30
350 Asp Tyr Thr Leu Phe Asn Leu Ile Pro Val Gly Leu Arg Val Val Ala
351 35 40 45
353 Ile Gln Gly Val Lys Ala Ser Leu Tyr Val Ala Met Asn Gly Glu Gly
354 50 55 60
356 Tyr Leu Tyr Ser Ser Asp Val Phe Thr Pro Glu Cys Lys Phe Lys Glu
357 65 70 75 80
359 Ser Val Phe Glu Asn Tyr Tyr Val Ile Tyr Ser Ser Thr Leu Tyr Arg
360 85 90 95
362 Gln Gln Glu Ser Gly Arg Ala Trp Phe Leu Gly Leu Asn Lys Glu Gly
363 100 105 110
365 Gln Ile Met Lys Gly Asn Arg Val Lys Lys Thr Lys Pro Ser Ser His
366 115 120 125
368 Phe Val Pro Lys Pro Ile Glu Val Cys Met Tyr
369 130 135
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372 <211> LENGTH: 139
373 <212> TYPE: PRT
374 <213> ORGANISM: Homo Sapiens
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384 Asn Ser Thr Leu Phe Asn Leu Ile Pro Val Gly Leu Arg Val Val Ala
385 35 40 45
387 Ile Gln Gly Val Lys Thr Gly Leu Tyr Ile Ala Met Asn Gly Glu Gly
388 50 55 60
390 Tyr Leu Tyr Pro Ser Glu Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu
391 65 70 75 80

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VERIFICATION SUMMARY

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Input Set : A:\053884-5001.ST25.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date